PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/502,040

DATE: 07/29/2004
TIME: 15:45:40

Input Set : A:\63358.app
Output Set: N:\CRF4\07292004\J502040.raw

```
    3 <110> APPLICANT: Liao et al.
    5 <120> TITLE OF INVENTION: ALANINE 2,3-AMINOMUTASE
    7 <130> FILE REFERENCE: 63358-09
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/502,040
C--> 10 <141> CURRENT FILING DATE: 2004-07-19
   10 <150> PRIOR APPLICATION NUMBER: PCT/US03/01635
   11 <151> PRIOR FILING DATE: 2003-01-17
   14 <150> PRIOR APPLICATION NUMBER: US 60/350,727
   15 <151> PRIOR FILING DATE: 2002-01-18
   17 <150> PRIOR APPLICATION NUMBER: US 60/375,785
   18 <151> PRIOR FILING DATE: 2002-04-25
   20 <160> NUMBER OF SEQ ID NOS: 66
   22 <170> SOFTWARE: PatentIn version 3.1
   24 <210> SEQ ID NO: 1
   25 <211> LENGTH: 40
   26 <212> TYPE: DNA
   27 <213> ORGANISM: Artificial Sequence
   29 <220> FEATURE:
   30 <223> OTHER INFORMATION: PCR primer
   32 <400> SEQUENCE: 1
   33 gcgcgaggag gagttcatat gaaaaacaaa tggtataaac                40
   36 <210> SEQ ID NO: 2
   37 <211> LENGTH: 36
   38 <212> TYPE: DNA
   39 <213> ORGANISM: Artificial Sequence
   41 <220> FEATURE:
   42 <223> OTHER INFORMATION: PCR primer
   44 <400> SEQUENCE: 2
   45 cgggcaccgc ttcgaggcgg ccgcaccatt cgcatg                   36
   48 <210> SEQ ID NO: 3
   49 <211> LENGTH: 1416
   50 <212> TYPE: DNA
   51 <213> ORGANISM: Bacillus subtilis
   53 <400> SEQUENCE: 3
   54 ttgaaaaaca aatggtataa accgaaacgg cattggaagg agatcgagtt atggaaggac    60
   56 gttccggaag agaaatggaa cgattggctt tggcagctga cacacactgt aagaacgtta   120
   58 gatgatttaa agaaagtcat taatctgacc gaggatgaag aggaaggcgt cagaatttct   180
   60 accaaaacga tccccttaaa tattacacct tactatgctt ctttaatgga ccccgacaat   240
   62 ccgagatgcc cggtacgcat gcagtctgtg ccgctttctg aagaaatgca caaaacaaaa   300
   64 tacgatctgg aagacccgct tcatgaggat gaagattcac cggtacccgg tctgacacac   360
   66 cgctatcccg accgtgtgct gtttcttgtc acgaatcaat gttccatgta ctgccgctac   420
   68 tgcacaagaa ggcgcttttc cggacaaatc ggaatgggcg tccccaaaaa acagcttgat   480
   70 gctgcaattg cttatatccg ggaaacaccc gaaatccgcg attgtttaat ttcaggcggt   540
```

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 72 gatgggctgc tcatcaacga ccaaatttta gaatatattt taaaagagct gcgcagcatt    600
 74 ccgcatctgg aagtcatcag aatcggaaca agagctcccg tcgtctttcc gcagcgcatt    660
 76 accgatcatc tgtgcgagat attgaaaaaa tatcatccgg tctggctgaa cacccatttt    720
 78 aacacaagca tcgaaatgac agaagaatcc gttgaggcat gtgaaaagct ggtgaacgcg    780
 80 ggagtgccgg tcggaaatca ggctgtcgta ttagcaggta ttaatgattc ggttccaatt    840
 82 atgaaaaagc tcatgcatga cttggtaaaa atcagagtcc gtccttatta tatttaccaa    900
 84 tgtgatctgt cagaaggaat agggcatttc agagctcctg tttccaaagg tttggagatc    960
 86 attgaagggc tgagaggtca tacctcaggc tatgcggttc ctacctttgt cgttgacgca   1020
 88 ccaggcggag gaggtaaaat cgccctgcag ccaaactatg tcctgtcaca aagtcctgac   1080
 90 aaagtgatct taagaaattt tgaaggtgtg attacgtcat atccggaacc agagaattat   1140
 92 atccccaatc aggcagacgc ctattttgag tccgtttttcc ctgaaaccgc tgacaaaaag   1200
 94 gagccgatcg ggctgagtgc cattttttgct gacaaagaag tttcgtttac acctgaaaat   1260
 96 gtagacagaa tcaaaaggag agaggcatac atcgcaaatc cggagcatga aacattaaaa   1320
 98 gatcggcgtg agaaaagaga tcagctcaaa gaaaagaaat ttttggcgca gcagaaaaaa   1380
100 cagaaagaga ctgaatgcgg aggggattct tcatga                              1416
103 <210> SEQ ID NO: 4
104 <211> LENGTH: 60
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: PCR primer
111 <400> SEQUENCE: 4
112 tatcaattcg ttacaggcga tacatggcac gcttcggcgc gtgtaggctg gagctgcttc     60
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116 <211> LENGTH: 60
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: PCR primer
123 <400> SEQUENCE: 5
124 gatgtcgcgg ctggtgagta accagccgca gggataacaa catatgaata tcctccttag     60
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 20
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: PCR primer
135 <400> SEQUENCE: 6
136 ttaccgagca gcgttcagag                                                 20
139 <210> SEQ ID NO: 7
140 <211> LENGTH: 20
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: PCR primer
147 <400> SEQUENCE: 7
148 cacctggcgg tgacaaccat                                                 20
151 <210> SEQ ID NO: 8
152 <211> LENGTH: 60
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154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: PCR primer
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163 <210> SEQ ID NO: 9
164 <211> LENGTH: 60
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: PCR primer
171 <400> SEQUENCE: 9
172 ttacaacgtt accgggtgtt ctttctcgcc tttcttaaac catatgaata tcctccttag      60
175 <210> SEQ ID NO: 10
176 <211> LENGTH: 51
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: PCR primer
183 <400> SEQUENCE: 10
184 cacaaaacaa aatacgatat ggaagacccg ctccatgagg atgaagattc a              51
187 <210> SEQ ID NO: 11
188 <211> LENGTH: 51
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: PCR primer
195 <400> SEQUENCE: 11
196 tgaatcttca tcctcatgga gcgggtcttc catatcgtat tttgttttgt g              51
199 <210> SEQ ID NO: 12
200 <211> LENGTH: 28
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: PCR primer
207 <400> SEQUENCE: 12
208 gaatcaatgt tccgtatact gccgctac                                        28
211 <210> SEQ ID NO: 13
212 <211> LENGTH: 28
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: PCR primer
219 <400> SEQUENCE: 13
220 gtagcggcag tatacggaac attgattc                                        28
223 <210> SEQ ID NO: 14
224 <211> LENGTH: 31
225 <212> TYPE: DNA
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226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: PCR primer
231 <400> SEQUENCE: 14
232 gttcctacct ttgttgtaca cgcaccaggc g                        31
235 <210> SEQ ID NO: 15
236 <211> LENGTH: 31
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: pcr primer
243 <400> SEQUENCE: 15
244 cgcctggtgc gtgtacaaca aaggtaggaa c                        31
247 <210> SEQ ID NO: 16
248 <211> LENGTH: 23
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR primer
255 <220> FEATURE:
256 <221> NAME/KEY: misc_feature
257 <222> LOCATION: (1)..(23)
258 <223> OTHER INFORMATION: y is t/u or c; s is g or c; b is g, c or t/u.
261 <400> SEQUENCE: 16
262 ttyatyggby tsggbaayat ggg                                 23
265 <210> SEQ ID NO: 17
266 <211> LENGTH: 20
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: PCR primer
273 <220> FEATURE:
274 <221> NAME/KEY: misc_feature
275 <222> LOCATION: (1)..(20)
276 <223> OTHER INFORMATION: y is t/u or c; s is g or c; b is g, c or t/u; w is a or t/u;
n is
277          a, c, g or t/u.
280 <400> SEQUENCE: 17
W-->  281 gaygcnccng tbwssggbgg                                     20
284 <210> SEQ ID NO: 18
285 <211> LENGTH: 21
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: PCR primer
292 <220> FEATURE:
293 <221> NAME/KEY: misc_feature
294 <222> LOCATION: (1)..(21)
295 <223> OTHER INFORMATION: y is t/u or c; r is g or a; n is a, c, g or t/u.
298 <400> SEQUENCE: 18
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RAW SEQUENCE LISTING   DATE: 07/29/2004
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        Input Set : A:\63358.app
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```
W--> 299 catrttrttr caratyttng c                                    21
    302 <210> SEQ ID NO: 19
    303 <211> LENGTH: 27
    304 <212> TYPE: DNA
    305 <213> ORGANISM: Artificial Sequence
    307 <220> FEATURE:
    308 <223> OTHER INFORMATION: PCR primer
    310 <400> SEQUENCE: 19
    311 ggtttacgag ggcgagaacg gcttgct                                27
    314 <210> SEQ ID NO: 20
    315 <211> LENGTH: 1416
    316 <212> TYPE: DNA
    317 <213> ORGANISM: Bacillus subtilis
    319 <220> FEATURE:
    320 <221> NAME/KEY: CDS
    321 <222> LOCATION: (1)..(1416)
    322 <223> OTHER INFORMATION:
W--> 325 <400> 20
    326 atg aaa aac aaa tgg tat aaa ccg aaa cgg cat tgg aag gag atc gag   48
    327 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
    328 1               5                   10                  15
    330 tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag   96
    331 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
    332             20                  25                  30
    334 ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat  144
    335 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
    336             35                  40                  45
    338 ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc  192
    339 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
    340     50                  55                  60
    342 ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat  240
    343 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
    344 65                  70                  75                  80
    346 ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg  288
    347 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
    348             85                  90                  95
    350 cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat  336
    351 His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp
    352             100                 105                 110
    354 tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt  384
    355 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
    356             115                 120                 125
    358 ctt gtc acg aat caa tgt tcc gtg tac tgc cgc tac tgc aca aga agg  432
    359 Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
    360             130                 135                 140
    362 cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat  480
    363 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
    364 145                 150                 155                 160
    366 gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta  528
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/29/2004
PATENT APPLICATION: **US/10/502,040**   TIME: 15:45:41

Input Set : **A:\63358.app**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 6,9
Seq#:18; N Pos. 19

VERIFICATION SUMMARY   DATE: 07/29/2004
PATENT APPLICATION: **US/10/502,040** TIME: 15:45:41

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```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:325 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:322
L:585 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:582
L:685 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:682
L:1104 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:1101
L:1473 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:1470
L:1879 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:53,Line#:1876
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